

Abstract

A method for the analysis of cytosine methylations in DNA is described. Here, the DNA to be investigated is first chemically or enzymatically converted. Then a promoter is introduced into the DNA. After this, the DNA is converted to RNA. The methylation pattern of the DNA can be concluded in different ways by means of an analysis of the RNA. The RNA is preferably fragmented chemically or enzymatically prior to the analysis, whereby the fragmenting results depend on the methylation pattern of the DNA. The method according to the invention is particularly suitable for the diagnosis and prognosis of cancer disorders and other diseases associated with a modification of the methylation pattern.